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Run
                                                                                                                                                                                                     Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                      Score
 SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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131.466 Million cell updates/sec
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                          sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_bacteriap:*
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sp_phage:*
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sp_mhc:*
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                                                                                                                                                                  Q8XA65
Q8FLC5
                                                                                                                                                                                                                                         SUMMARIES
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QBxa65 escherichia
QBflc5 escherichia
Q7udui shigella fl
QB13d3 colwellia m
QBzim6 yersinia pe
QB3mh4 shigella fl
QBdf67 vibrio vuln
QB7rx2 vibrio para
Q93s23 rhizobium t
Q92t07 rhizobium m
Q99dd2 rhizobium l
QBye77 brucella me
QBye77 brucella su
QBye77 brucella su
QBrb67 thermoanaer
Q7vql3 candidatus
QB9au7 buchnera ap
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56	56	56	56	56	56	56	57	57	57	58	58	58	59	60	60	60	60	60	61	62	63	63	63	63	64	65	66	69
69.1		69.1		69.1	69.1	69.1	70.4	٠	70.4	71.6	71.6	71.6	72.8	74.1	74.1	74.1		74.1						•	•			
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Q8E7Q7	Q879J5	Q8NZM7	Q99YC9	Q9FAZ9	Q8DWH2	Q8CWT2	Q818F0	Q81LS3	QBNK58	Q8LEU4	Q93Q66	Q88DU3	Q8XW41	Q7UM96	QBPAK8	Q9APF2	Q8PMA9	Q92J37	Q8XIT1	Q87WP1	Q835R5	Q7VVY3	Q7W520	Q7WGI5	QBRH03	Q8D2Q6	Q93R26	Q8KYX6
Q8e7q7 streptococc		Ø	Ø	St	\sim			Q811s3 bacillus an	77	4		Q88du3 pseudomonas			xanthomona	~	Q8pma9 xanthomonas	Q92j37 rickettsia				Q7vvy3 bordetella					٠,	Q8kyx6 uncultured

ALIGNMENTS

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	"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";	Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinaqawa H.;	Kurokawa K., Ishii K., Yokoyama , Murata T., Tanaka M., Tobe T.,	This workship	SEQUENCE FROM N.A.	Nature 409:529-533(2001). [2]	"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";	Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz J.C.,	Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,	Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,	Perna N.T., Plunkett G. III, Burland v., Mad b., Glasket C.B., Rose D.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,		STRAIN=0157:H7 / EDL933 / ATCC 700927;	SEQUENCE FROM N.A.	NCBL IdXID=63334;	Enterobacteriaceae; Escherichia.	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			U	(TrEMBLrel. 20,	20, Created)	QBXA65 ERBHILINAKI; ERI; 3/0 Am.		

100.0 100.0 96.3 96.3 95.1 95.1 90.1 90.1 88.9 86.4

Q93S23
Q93S25
Q92T07
Q92T07
Q8YE77
Q8FXX1
Q8RB67
Q8RB67
Q8RB67
Q7VQL3

6 Q7UDU1 Q8L3D3 5 Q8ZIM6 5 Q83MH4 5 Q8DF67

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XX MEDLINE-22388234; PubMed=12471157;

XA MEDLINE-22388234; PubMed=12471157;

XA Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

XA Mayhew G.F., Rose D.J., Liou S.-R., Boutin A., Hackett J., Stro

XA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

XI Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

XI Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

XI McMayhew G.F., Rose D.J., Schwartz D.C., Perna N.T.,

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XI McMayhew G.F., Rose D.J., Schwartz D.C., Perna N.T.,

XI McMayhew G.F., Rose D.J., John S., Schwartz D.C., Perna N.T.,

XI McMayhew G.F., Rose D.J., John S., Schwartz D.C., Perna N.T.,

XI McMayhew G.F., Rose D.J., John S., Schwartz D.C., Perna N.T.,

XI McMayhew G.F., Rose D.J., John J. N.

XI McMayhew G. McM
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Best Local S
Matches 15
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00190; CYTOCHROME_C;
                                                                 Pfam; PF00226; DnaJ; 1.—
Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGXG;
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01-OCT-2003 (TrEMBLrel.
Chaperone protein dnaJ.
DNAJ OR C0020
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01-MAR-2003
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90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00190; CYTOCHROME C; 2. PROSITE; PS00636; DNAJ 1; 1. PROSITE; PS50076; DNAJ 2; 1. PROSITE; PS00637; DNAJ CXXCXGXG; 1. Heat shock; Complete proteome.
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Pfam; PF01556; DnaJ C; 1.
Pfam; PF00684; DnaJ CXXCXGXG;
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
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GO; GO:0003773; F:heat shock protein activity; IEA.
GO; GO:0006118; F:electron transport; IEA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR00239; DnaJ_C.
InterPro; IPR001305; DnaJ_C.
InterPro; IPR001305; DnaJ_C.
InterPro; IPR001305; DnaJ_C.
InterPro; IPR001305; DnaJ_N.
InterPro; IPR003095; HSP_DnaJ_pep.
InterPro; IPR003095; HSP_DnaJ_pep.
InterPro; IPR003095; HSP_DnaJ_pep.
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GO:0005489;
GO:0003773;
GO:0006118;
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376 AA; 41044 MW;
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RESULT 4

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ID QBL3D3

AC QBL3

AC QBL3

DT 01-C

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ID Q7UDU1,
AC Q7UDU1,
DT 01-OCT-
DNAJ OF
OS Shigell
OC Bacterok
OX NCBI-Ta
RN (1]-
RN SEQUENC
RC STRAIN-
RA FOURTIÉ
RA MEDLINE
RA FOURTIÉ
RA MAU B.,
RA FOURTIÉ
RA MAU B.,
RA SCHWART
RI LINFERT
RI INFECT.
DR EMBL; &
WHEAT S!
SQ SEQUENC
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Matches 15
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Best Local
                                     SEQUENCE FROM N.A.

Yamauchi S., Okuyama H., Nishiyama Y., Hayashi H.;

"Cloning and transcriptional regulation of dnak and dnak
psychrophilic bacterium, Colwellia maris.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7UDU1;
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Heat shock protein 40.
                              EMBL; AB084455;
                                                                                                                                                                                               Alteromonadaceae;
NCBI_TaxID=77524;
                                                                                                                                                                                                                                            Colwellia maris (Vibrio sp. (strain ABE-1)).
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                     Colwellia maris (Vibrio
                                                                                                                                                                                                                                                                                                   DNAJ
                                                                                                                                                                                                                                                                                                                                                                                                                    Q8L3D3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22590274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., D. Wei J., Goldberg M.B., Burland V., Venkatesan M.M., D. Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence and comparative flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
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PROSITE; PS50076; DNAJ_2; 1.

PROSITE; PS00637; DNAJ_CXXCXGXG;

Complete proteome.

SEQUENCE 376 AA; 41044 MW; 81
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     shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCC 700930 / Serotype 2a;
                                                                                                                                                                                                                        Colwellia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41072 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; =-
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Last
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                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1B354AC3F9844532
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                                                                                                                                                                                                                                                                                                                                         sequence update) annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomics of Shigella
                                                                                                  dnaK and dnaJ
                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                              Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deng W.,
J., Darling i
                                                                                             genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT TO RESULT TO THE PROPERTY OF THE PROPER
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STRAIN-CO-92 / Biovar Orientalis;
STRAIN-CO-92 / Biovar Orientalis;
MEDLINE-Z1470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Baker S., Basham D., Bentley S.D., Brooks F., Dougan G.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford M.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford M.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford M.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford M.,
Leather S., Moule S., Oyston P.C.F., Quail M., Ru
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chaperone protein DnaJ (Chaperone with DnaK, heat shock protein)
DNAJ OR YPO0469 OR Y3705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBDLINE=22137863; PubMed=12142430;

Deng W., Burland V., Piunkett G. III, Boutin A., Mayhew

Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8ZIM6
                                                                                                                                                            PRINTS; PRO0625; DNĀJPROTEIN.
PROSITE; PS00190; CYTOCHROME C; 2.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008971;
InterPro; IPR003095;
Pfam; PF00226; DnaJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR002939; Dnad_C.
InterPro; IPR001305; Dnad_CXXCXGXG.
InterPro; IPR001623; Dnad_N.
InterPro; IPR008971; HSP40_Dnad_pep.
InterPro; IPR008971; HSP40_Dnad_pep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Yersinia pestis KIM.", J. Bacteriol. 184:4601-4611(2002). EMBL; A.414142; CAC89325.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-KIMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:523-527(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       υī
y Match
Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0005489; F:electron transporter activity; GO:0003773; F:heat shock protein activity; IF GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB0058; AB0058
                                                                                                                                       shock;
                                                                                                                                                                                                                                                                                                                               PF01556; DnaJ_C; 1.
PF00684; DnaJ_CXXCXGXG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
IM5 / Biovar Mediaevalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKRAAYDQYGHAAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKRAAYDQYGHAAFE
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                                                                                                    Complete proteome.
379 AA; 41278 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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   100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
Score 81;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58A2894D13F8E9FA CRC64;
                                                                                                    AC1922FC3D707C93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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      DB 16;
1.3e-05;
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InterPro; IPR001305; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR0018971; HSP40 DnaJ_pep.
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Shigella flexneri.
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EMBL; AP005075; BAC58017.1; -.
GO; GO:0003754; F:chaperone activity; IEA.
GO; GO:0005489; F:electron transporter activity;
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR000345; DnaJ_C.
InterPro; IPR001305; DnaJ_C.
InterPro; IPR001305; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
                                                                                                                                                                                                                             STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDINB=22509454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361.743-749(2003).
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GO; GO:0003754; F:chaperone activity; IEA.
GO; GO:0005489; F:clectron transporter activity; IEA.
GO; GO:0005489; P:electron transport; IEA.
InterPro; IPR00345; CytC_heme_BS.
InterPro; IPR00345; CytC_heme_BS.
InterPro; IPR003935; DnaJ_CXXCXGXG.
InterPro; IPR001305; DnaJ_CXXCXGXG.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR008971; HSP40_DnaJ_pep.
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01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
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Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGXG;
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InterPro; IPR003095;
Pfam; PF00226; DnaJ;
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Choy H.E.;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41226 MW;
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93.3%;
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Pred. No.
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                                                   Query Match
Best Local S
Matches 14
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C -!- SIMILARITY: BELONGS TO THE DNAJ FAMILY.

R EMBL; AJ311186; CAC38775.1; -.

R GO; GO:0003754; F:chaperone activity; IEA.

R GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0006489; F:electron transporter activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0006118; CycC heme BS.

R InterPro; IPR00345; CytC heme BS.

R InterPro; IPR00345; CytC heme BS.

R InterPro; IPR00393; DnaJ_C.

R InterPro; IPR001053; DnaJ_C.

R InterPro; IPR001603; DnaJ_C.

R InterPro; IPR001603; DnaJ_DaJ_Dep.

InterPro; IPR001603; HSP40_DnaJ_Dep.

R InterPro; IPR001603; HSP40_DnaJ_Dep.

R InterPro; IPR001603; HSP40_DnaJ_Dep.

R InterPro; IPR001603; DnaJ_C; 1.

R Pfam; PF00156; DnaJ_C; 1.

R Pfam; PF00156; DnaJ_C; 1.

R Pfam; PF001604; DnaJ_CXXCXXXX; 1.
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Best Local
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Pfam; PF01556; DnaJ C; 1.
Pfam; PF01654; DnaJ C; 1.
Pfam; PF00684; DnaJ CXXCXGXG; 1.
PRINTS; PR00625; DNAJPROTEIN.
PROSITE; PS00190; CYTOCHROME C; 2.
PROSITE; PS00365; DNAJ 1; 1.
PROSITE; PS00637; DNAJ CXXCXGXG; 1.
                                                                                                                Chaperone;
NON_TER
NON_TER
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01-DEC-2001
01-OCT-2003
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Q93S23;
                                                                                                       SEQUENCE
                                                                                                                                                      PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS00637; DNAJ CXXCXGXG;
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SEQUENCE
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PROSITE; PS00636;
                                                                                                                                                                                                              SMART; SM00271; DnaJ; 1
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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                                                                                                                                                                                                                         PRINTS; PR00625; DNAJPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CIAT899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=398;
                                                                                                                                                                                                                                                                                                                                                                                                                                        egume symbiosis."
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39
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                                                              Similarity
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                        OKRAAYDOYGHAAFE 15
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                                                                                                                                           Repeat.
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                                                                                                     331 AA;
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                                                                                                                    331
                                                   Conservative
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                                                                                                                                                                                          CYTOCHROME_C;
                                                                                                     35577 MW;
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                                                              95.1%;
93.3%;
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93.3%;
53
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                                                Score 77; DB Pred. No. 5.4e
1; Mismatches
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Pred. No. 4.2e-05;
1; Mismatches (
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                                                               5.4e-05;
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RESULT 10
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RESULT
Q98DD2
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Best Local
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591782; CAC41570.1; -.
GO; GO:0003754; F:chaperone activity; IEA.
GO; GO:0005489; F:electron transporter activity;
GO; GO:0006118; P:electron transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00636; DNAJ_1; 1.

PROSITE; PS00636; DNAJ_2; 1.

PROSITE; PS50076; DNAJ_2; 1.

PROSITE; PS00637; DNAJ_CXXCXGXG;
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01-DEC-2001
                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                       Rhizobium
                                                                                                                                                                                                                                                                          Heat
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                           Q98DD2;
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00625; DNAJ; SMART; SM00271; DnaJ;
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium
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                                   SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q98DD2
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InterPro; IPR002939; DnaJ_C.
InterPro; IPR001305; DnaJ_CXXCXGXC
InterPro; IPR001623; DnaJ_N.
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       STRAIN=MAFF303099;
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PF01556; DnaJ_C; 1.
PF00684; DnaJ_CXXCXGXG; 1.
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IPR001623;
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1 (TremBLrel. 18,
3 (TremBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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93.3%;
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Pred. No. 6.2e-05;
1; Mismatches 0
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PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
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EMBL; AE009632; AAL53182.1;
PIR; AC3502; AC3502.
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Watanabe A., Idesawa K., Ishi
Kishida Y., Kiyokawa C., Koha
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01-OCT-2003 (TrEMBLrel.
Chaperone protein DNAJ.
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GO; GO:0005489; F:electron transporter
GO; GO:0006118; P:electron transport; 1
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Brucellaceae; Brucella.
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InterPro; IPR008971;
InterPro; IPR003095;
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InterPro; IPR001305;
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Takeuchi C., Yamada M.,
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  GO; GO:0003754; F:chaperone activity; 1
GO; GO:0005489; F:electron transporter
GO; GO:0006118; P:electron transport; 1
InterPro; IPR000345; CytC.heme_BS.
InterPro; IPR002939; DnaJ_C.
InterPro; IPR001305; DnaJ_CXXCXGXG.
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PF01556; DnaJ_C;
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SM00271; DnaJ; 1.
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13; Conserv
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DnaJ_N.
HSP40_D
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S., Nakazaki
Tabata S.,
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Pred. No.
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Matsumoto M., Matsuno
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K., Kimura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E. Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M., "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.", Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002). EMBL, AC3502, AC3502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00625; DNĀJPROTEIN.

SMART; SM00271; DNĀJ; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00636; DNĀJ_1; 1.

PROSITE; PS00637; DNĀJ_CXCXGXG; 1.

COMPLETE PROFICE 377 AA; 41078 MW; E66AAlF16606E775 CRC64;
                                                                                                                                                                                                                             Pfam; PF00226; DnaJ; 1.

Pfam; PF01556; DnaJ_C; 1.

Pfam; PF00684; DnaJ_CXCXGXG; 1.

PRINTS; PR00625; DNAJPROTEIN.
                                                                                                                                                                                                                                                                                                                           GO; GO:0003754; F:chaperone activity; IEA.
GO; GO:000548); F:electron transporter activity;
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR002939; DnaJ_C.
InterPro; IPR002939; DnaJ_CXC.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR0010523; Hsp_DnaJ.
                                                                                                  PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                             SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22247741; PubMed=12271122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brucella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chaperone protein DnaJ.
DNAJ OR BR2126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8FXX1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00226; DnaJ; 1.
Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGXG;
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InterPro; IPR003095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Biovar 1;
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                                                        41078 MW;
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86.7%;
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Hsp_DnaJ.
     90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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     Score 73;
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Pred. No. 0.
                                                        E66AA1F16606E775 CRC64;
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0.0003;
     DB 16;
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Length 377;
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RESULT 15
Q7VQL3
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Q8RB67
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A Tran H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:69-700(2002).

R EMBL, AE013061; AAM24212.1; -.

R GO; GO:000514; F:chaperone activity; IEA.

R GO; GO:0006118; F:electron transporter activity; IEA.

R GO; GO:000618; F:electron transport; IEA.

R GO; GO:000618; F:electron transport; IEA.

R InterPro; IPR00345; CytC_heme_BS.

R InterPro; IPR00395; DnaJ_CXCXCXGXG.

R InterPro; IPR001305; DnaJ_N.

R InterPro; IPR001623; DnaJ_N.

R InterPro; IPR001623; DnaJ_N.

R InterPro; IPR001623; DnaJ_N.

R Dfam. Defn0796; NpaJ C.

R Dfam. Defn0796; NpaJ C.
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Best Local
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                                                                                                                                                                              Q7VQL3;
01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                        DnaJ protein.
DNAJ OR BFLI15.
Candidatus Blochmannia floridanus.
Bacteria; Proteobacteria; Gammapro
Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
NCBI_TaxID=203907;
[1]
                                                                                                                                                                                                                                                                                    Q7VQL3
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PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS0076; DNAJ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00226; DnaJ; 1. Pfam; PF01556; DnaJ_C; 1. Pfam; PF00684; DnaJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter tengcongensis.

Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; PubMed=11997336;
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003
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                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 AA; 42718 MW;
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(TrEMBLrel. 25, Last annotation update)
hanerones (contain C-terminal Zn finger domain)
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                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                     Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                 Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72; DB 16;
Pred. No. 0.00046;
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RP SEQUENCE FROM N.A.

RX MEDLINE=22784745; PubMed=12886019;
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
RA Gil R., Silva F.J., Genzalez-Candelas F., Genzalez-Candelas F.,
RA Gil R., Silva F.J., Genzalez-Candelas F.,
RA Gil R., Silva F.J., Genzalez-Candelas F., Genzalez-Candelas F.,
RA Gil R., Silva F.J., Genzalez-Candelas F., Genzalez-Candelas F.,
RA Gil R., Silva F.J., Genzalez-Candelas F., Genzalez-Candelas F.,
RA Gil R., Silva F.J., Genzalez-Candelas F., Genzalez-Candelas F.,
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1: pir1:*
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45	44	4.	42	41	40	39	38	37	36	ω U	34	ω u	32	31	30
48	49	49	49	50	50	50	50	50	52	52	52	53	95	56	56
59.3	60.5	60.5	60.5	61.7	61.7	61.7	61.7	61.7	64.2	64.2	64.2	65.4	69.1	69.1	69.1
380	498	375	370	416	383	379	348	297	389	376	372	499	378	372	368
2	N	Ν	N	N	N	N	N	Ν	2	2	N	N	N	N	N
JC4739	T06594	D82894	D83818	F71379	E90603	в89939	T04618	G81329	S41748	H69038	B41874	G96831	D95060	H97928	F82570
shock	shock		-shock				heat shock protein	able c	shock	shock	heat shock protein	hypothetical prote	dnaJ protein [impo	heat-shock protein	DnaJ protein XF233

ALIGNMENTS

HHECDJ

heat shock protein dnaJ - Escherichia coli (strain K-12)
(;Specles: Escherichia coli
(;Specles: Escherichia coli
(;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 01-Mar-2002
(;Accession: A92572; A26298; S40537; G64721; A26299
R;Bardwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zylicz, M.; Georgopoulos, C.
J. Biol. Chem. 261, 1782-1785, 1986
A;Title: The nucleotide sequence of the Escherichia coli K12 dnaJ gene.
A;Reference number: A92572; MUID:86111850; PMID:3003085
A;Accession: A92572

A; Molecule type: DNA A; Residues: 1-376 < BAR>

A;Cross-references: GB.M12565; NID:g145767; PIDN:AAA23693.1; PID:g145769
A;Experimental source: strain K12
R;Ohki, M.; Tamura, F.; Nishimura, S.; Uchida, H.
J. Biol. Chem. 261, 1778-1781, 1986
A;Title: Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the A;Reference number: A26298; MUID:86111849; PMID:3003084

A;Molecule type: DNA A;Residues: 1-376 <OHK> A; Accession: A26298

A;Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; GR;Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizob submitted to the EMBL Data Library, December 1992

A; Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-A; Reference number: 840531A; Accession: S40537

A;Molecule type: DNA A;Residues: 1-376 <YUR>

A;Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01292.1; PID:g216441
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; May, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503

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A;Accession: G64721

A;Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA A; Residues: 1-376 <BLAT>

A;Cross-references: GB:AE000112; GB:U00096; NID:g1786192; PIDN:AAC73126.1; PID:g1786197, A;Experimental source: strain K-12, substrain MG1655 C;Coment: This protein is induced by heat shock under the control of the htpR gene proc

C; Genetics:

A;Gene: dnaJ

A;Map position: 0 min C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology C;Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein F;5-70/Domain: dnaJ amino-terminal homology <DNJ>

F;77-106/Region: G/F moti F;144-151/Region: CXXCXGX CXXCXGXG repeat

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F;183-190/Region: CXXCXGXG
F;197-204/Region: CXXCXGXG
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                                                                                                                                                                                                                                                                                                                                                                             C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Datecession: G85481 C;Accession: G85481 C;Accession: Flunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: G90630
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C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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A;Experimental source: strain O157:H7, substrain EDL933
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Best Local S
Matches 15
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M.; Shinagawa,
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A; Title: Whole-genome random sequencing
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RESULT 4

Small, K.V.; and assembly

Fraser, of Haemo

Haemophilus

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chaperone protein DnaJ [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0058
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heat shock protein dnaJ - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999

C;Accession: C64112

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A., Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A., Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A., Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A., Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A., A., Title, McDonald, L.A.; Smith, McDon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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C;Superfamily: heat shock protein dnad; dnad amino-terminal homology
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A; Residues: 1-379 < KUR>
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C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Authors: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608
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, S.; Moule, S.; O'Gaora,
Nature 413, 848-852, 2001
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A; Residues: 1-379 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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Davis, P.; Davies, R.M.; Dowd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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e, N.; Farrar,
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RESULT 8
S15295
nolC prot
                                        R;Krishnan, H.B.; Pueppke, S.G.
Mol. Microbiol. 5, 737-745, 1991
A,Title: nolc, a Rhizobium fredii gene involved in cultivar-specific nodulation of soybe
A,Reference number: S15295; MUID:91260457; PMID:1646377
A;Accession: S15295
A;Status: preliminary
A;Status: preliminary
                                                                                                                                      nolC protein - Rhizobium fredii
C;Species: Rhizobium fredii
C;Date: 21-Nov-1993 #sequence_revision
C;Accession: S15295
R;Krishnan, H.B.; Pueppke, S.G.
             A; Molecule type: DNA
A; Residues: 1-392 < M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-381 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: DNA Sequence of both chromosomes of the cholera A; Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dnaJ protein VC085
C; Species: Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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F;89-121/Region: G/F motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Start codon: C; Superfamily:
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A;Accession: C64112
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Matches 15
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Best Local :
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;Superfamily: heat shock
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CXXCXGXG repeat
CXXCXGXG repeat
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93.3%;
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Pred. No.
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Pred. No. 1.7e-06;
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H.; Dragoi, I.; Sellers,
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F;77-108/Region: G/F motif
F;145-152/Region: CXXCXXXX
F;162-169/Region: CXXCXXXX r
F;184-191/Region: CXXCXXXX r
F;198-205/Region: CXXCXXXX r
                                                                                                            A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-377 <STO>
A; Cross-references: GB: AP000398; (A)
                                                                A;Gene: dnaJ; I
C;Superfamily:
                                                                                                                                                                                                                                                                             dnaJ protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                          A; Accession: F84947
                                                                                                                                                                                                         A; Title: Genome sequence of A; Reference number: A84930;
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                                                                                                                                                                                                                                           Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                     R;Shigenobu, S.;
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                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology C;Keywords: DNA replication; heat shock; molecular chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Sato, S.; Ishikawa, H.
J. Biochem. 122, 41-48, 1997
A;Title: Structure and expression of the dnakJ operon of A;Reference number: JC5608; MUID:97420684; PMID:9276669
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JC5609
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A; Residues: 1-377 <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Buchnera sp.
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
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Best Local :
                                                                                 dnaJ; BU152
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      13;
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                                                               heat shock protein dnaJ;
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86.7%;
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93.3%;
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   2;
                 Score 75;
Pred. No.
                                                                                                                              GSPDB: GN00144
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Pred. No. 1
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l; Mismatches
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QKRAAYDQYGHAAFE 15

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
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                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Cellier, M.F.; Teyssier, J.; Nicolas, M.; Liautard, J.P.; Marti, J.; Sri Widada, J. J. Bacteriol. 174, 8036-8042, 1992
A;Title: Cloning and characterization of the Brucella ovis heat shock protein DnaK funct A;Reference number: A47042; MUID:93094135; PMID:1459952
A;Accession: B47042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: dnaJ; NMB0059; NMADZUY
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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                                                    C;Superfamily: heat shock protein d
C;Keywords: DNA replication; heat s
F;4-69/Domain: dnaJ amino-terminal
F;76-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;163-170/Region: CXXCXGXG repeat
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A;Experimental source: serogroup A, strain Z2491
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                             ;Cross-references: EMBL:M95799; NID:g144114; PIDN:AAC36133.1; PID:g144116; Note: sequence extracted from NCBI backbone (NCBIN:119966, NCBIP:119968)
                                                                                                                                                                                                                                                                                                                                                           Molecule type: nucleic acid; Residues: 1-375 < CEL>
                                                                                                                                                                         Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology; Keywords: DNA replication; heat shock; molecular chaperone
                                                                                                                                                                                                                                      ;Gene: dnaJ
                                                                                                                                                                                                                                                                           ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999;Accession: B47042
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repeat
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chaperone protein dnaJ [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AC3502
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
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Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A;Reference number: AD3252; PMID:11756688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecular chaperone, DnaJ family dnaJ [imported] - Agrobacterium tumefaciens
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A;Cross-references: GB:AE008917; PIDN:AAL53182.1; PID:g17984054; GSPDB:GN00190
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                                                                                                                                                                                                                              C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-377 <KUR>
A;Cresidues: 1-377 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41146.1; PID:g17738442; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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Best Local Similarity
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M.; McClell:
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QKRAAYDRFGHAAFE

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Chaperone protein dnaJ [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep_2001 #sequence_revision 30-Sep_2001 #text_change 18-Nov-2002
C;Accession: D97373
R;Goodner, B;Hinkle, G;Gattung, S;Miller, N.;Blanchard, M.;Qurollo, B.;Goldman, A.;Liu, F;Wollam, C.;Allinger, M.;Doughty, D.;Scott, C.;Lappas, C.;Markelz, B.;
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Accession: D97373
A;Status: preliminary
A;Accession: D97373
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RESULT 1

AAW25795 standard; peptide;

AΑ

ALIGNMENTS

AAW25795;

06-APR-1998 (first entry)

Peptide dnaJp1 which protects against arthritogenic peptides

arthritogenic peptide; autoimmune disease; systemic anti-dnaupl antibody; passive immunisation; rheumatoid arthritis-susceptibility detection. dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine; immune system;

Escherichia coli.

WO9734002-AI

18-SEP-1997.

20-FEB-1997; 97WO-US002957

15-MAR-1996; 96US-00618464

(REGC) UNIV CALIFORNIA.

DA,

Albani S;

WPI; 1997-470882/43.

Vaccine for protecting against arthritogenic peptide(s) containing dnaJpl - also determining pre-disposition to rheumatoid arthritis by detecting anti-arthritogenic peptide antibodies.

Disclosure; Page 5; 44pp; English.

AAW25795
ID AAW2
XX
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PS Disc
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CC can Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to a induce relatively strong immune response in seropositive adult rheumatoid arthritis patients. This peptide was used in a vaccine for protecting against arthritogenic peptides. The vaccine contains a carrier, pure dnaJp1 peptide or a recombinant gene expression vector encoding the dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis or other autoimmune diseases). Vaccines can target the arthritogenic peptides before they are presented to the systemic immune system. Anti-dnaJp1 antibodies can also be used for passive immunisation. Antibodies be used ť detect rheumatoid arthritis-susceptibility sequences g

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RESULT 2
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                                                                                                         This peptide is derived from Escherichia coli heat shock protein dnaupl.

CC Novel artificial antigen presenting cells (APC) of the invention comprise

CC antigens, such as the present peptide, that are presented by a major

CC histocompatibility complex (MHC) component for contact with, and

CC recognition by, a T cell receptor. The invention is directed to

CC artificial APC and methods of making APC, which are used to isolate and

CC expand T cell populations and to modulate T cell responses. The invention

CC also provides novel methods for the identification and isolation and

CC injusomes containing MHC:peptide complexes, accessory molecules, co-

CC to T cell binding or modulation that are used in the binding of

CC artificial APC to solid support systems that may be used in the retrival

CC antidentification and antigen-specific T cells. Devices and methods are

CC and identification and antigen-specific T cells. Devices and methods are

CC cell response, e.g. autoimmune disorders (especially type I diabetes

CC mellitus, multiple sclerosis, rheumatoid arthritis, dermatomiosytis,

CC iuvenile rheumatoid arthritis, and uveitis). alleroies. cancer: viral
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                                                                                               juvenile rheumatoid arthritis and uveitis), allergies, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .g. autoimmune diseases, allergies.
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                                                                  graft rejection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorderal nervous system disease; cancer; melanoma; anti-melanoma vaccin human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a pharmaceutical compound (I) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MiC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomodulator, endocrine, antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stabilized pharmaceutical glutamine, useful e.g. in with strong acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM99341;
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                                                                                                   immune deficiency, autoimmune states, hypersensitivity, allergy, graft rejection, infection, hormonal disorders and central nervous system diseases), also, where (I) is a MHC ligand (Ia), in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections; or (ii) of cancers. A particular application is in antimelanoma vaccines. (I) are also useful for in vitro diagnosis of diseases associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                               neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 107; 149pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611470/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000FR-00003711.
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                                                                          can be used
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                                                                          in pharmaceutical compounds from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing N-terminal glutamic acid or anti-melanoma vaccines, is an addition
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); Mismatches 0;
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The invention relates to an artificial antigen presenting cell (I) C comprising liposome, major histocompatibility complex (MHC), antigen and cacessory molecule components. (I) is used in methods for the following: (2) identifying T cells specific for an antigen of interest; (2) (2) identifying T cells specific for an antigen of interest; (2) coll response; (4) characterising the functional state of antigen— Specific T cells; (5) treating a condition in a subject which would be certain antigen—specific T cells to increase T-helper (Th) 2 response condition for decrease Th1 response; (6) identifying antigen—specific T cells to increase T-helper (Th) 2 response condition for decrease Th1 response; (6) identifying antigen—specific T cells to increase T-helper (Th) 2 response condition for decrease Th1 response; and (7) treating antigen—specific T cells specific for epitopes on a graft donor's tissue likely to elicit graft conditions in sustain for treating autoimmune disease such as type I condition to the suseful for treating autoimmune disease such as type I condition to the suseful for treating autoimmune disease such as type I condition by a sustain for treating allergy due to allergens such as dust, animal condition by as well as co-stimulatory molecules, and other proteins in the liposomes allow for substantially improved binding association and manipulation of T cells which is very important concerned to in the identification and stimulation of antigen—specific T cells. The proteins in the identification and stimulation of antigen—specific T cells. The concerned to the conc
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Matches :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New artificial antigen presenting cell, useful for modulating T cell response for treating allergies and cancers, comprises liposome, major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigenic; antidiabetic; neuroprotective; antirheumatic; antiarthritic; dermatological; immunosuppressive; ophthalmological; antiallergic; cytostatic; virucide; antibacterial; artificial antigen presenting cell liposome; major histocompatibility complex; MHC, T cell; allograft; cytokine production; T-helper 2 response; transplantation therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease; type I diabetes mellitus; multiple sclerosis; arthritis; dermatomyositis; juvenile rheumatoid arthritis; lergy; cancer; infection; dnaupl heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
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represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complex,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen and accessory molecule components.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 response; transplantation therapy;
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RESULT 5
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                                                                                                                                          This invention relates to the use of a peptide, which is an immunoger portion derived from a dnaJ heat shock protein (hsp) in modulating ar immune response in a subject. The peptides of the invention may have immunomodulatory, cytostatic, antiinflammatory, antibacterial or
                                                                                                                                                                                                                                 New immunomodulatory peptides from heat shock proteins, useful treating immunological disorder in subjects such as humans, e.
                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; arthritis; articular juvenile idiopathic arthritis; infectious disease; inflammatory bowel disease; cancer; HDJ2; mucosal tolerisation; DNA vaccination; anergy induction.
                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                     Martini
                                                                                                                                                                                                                                                                                                                                 01-NOV-2000; 2000US-0245181P
                                                                                                                                                                                                                                                                                                                                                    31-OCT-2001; 2001WO-US045344
                                                                                                                                                                                                                                                                                                        (MART/)
                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli DNAJ
                                                                                                                                                                                                                          immune disease (e.g. arthritis),
                                                                                                                                                                                                                                                                  2002-489999/52
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                                                                                                                                                                                                                                                                                                                UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKRAAYDQYGHAAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKRAAYDQYGHAAFE
                                                                                                                                                                                               Page 53; 84pp;
                                                                                                                                                                                                                                                                                    Albani
                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory; antibacterial; antiarthritic; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PI immunogenic
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                                                                                                                                                                                                                   or cancer
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                                                                                                                                                                                                                                                                                    Carson
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                                                                                                                                                                                                                                                                                  DA,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                  Prakken BJ;
                                                                                                                                                                                                                            infectious
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s 0;
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د
                                                                                                                                                                                                                          disease,
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antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating (i.e. augmenting/inducing reducing/inhibiting) an immune response in a subject having an immunological disorder (e.g. autroimmune disease such as arthritis or articular juvenile idiopathic arthritis) an infectious disease, an inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunoeffector cell

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responsiveness in a subject. The immunogenic peptide is particularly

ul for treating the above-mentioned diseases in mammals, e.g. horse, farm animal (e.g. ovine, bovine or porcine) or human ral, the peptide is useful in methods involving mucosal toler vaccination, anergy induction or active immunisation. The presence represents the E.coli DNAJ PI immunogenic peptide of the

tolerisation e.g.

DNA vaccination, anergy sequence represents the

SQ

Sequence

5

AA;

Matches Query Match

POCAT 15;

Similarity

100.0%;

Score 81; Pred. No.

9.8e-08; DB 5; 0

Length 15 Indels

Conservative

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                                                                                                                                                                                                                                                                                            The invention relates to human leukocyte antigen (HIA) pan DR-binding peptide comprising a fragment of a stress protein that binds to one or more major histocompatibility complex (MHC) class II molecules. The invention also relates to heat shock protein (hsp) peptides. The peptides of the invention and thr immunomodulating composition comprising these peptides are useful for modulating, treating or preventing an immune-mediated disease in a mammalian subject e.g. human, having or at risk of having a disease including autoimmune disease, multiple sclerosis (MS), rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I diabetes, scleroderma, ulcerative coiltis, cancer (e.g. melanoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours, lupus are transcribed to the sclerosis in the coiltis of the sclerosis in the sclerosis 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human heat shock protein (hsp) dnaJP1 peptide.
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retinoblastoma, sarcoma and connective tissue cancers) and infectious diseases. The peptides of the invention are also useful for screening peptides or analogues that modulate pathogenic immune response. These peptides are useful for treating autoimmune diseases or disorders including Sjogren's syndrome, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2000;
06-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human leukocyte antigen pan DR-binding peptide, useful for treating immune mediated diseases and conditions, has a fragment of stress protein that binds to major histocompatibility complex class II molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 45; 68pp; English
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2001US-00828574.
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen-specific epitope; immune response; T cell; cytokine; antiarthritic; antidiabetic; neuroprotective; anti-inflammatory; cytostatic; antithyroid; anti-asthmatic; immunosuppressive; antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
                                                                                         in a subject having an immune-related disorder. The method comprises administering an antigen-specific epitope, where administration prove epitope-specific T cell immune modulation; and (b) administering a cytokine, an agent that effects cytokine activity or expression, or anticytokine therapy. The method of the invention has antiarthritic, antidiabetic, neuroprotective, anti-inflammatory, cytostatic, anti-sthmatic, immunosuppressive, antipsoriatic, anti-dermatological, and antipsoriatic activity. The method is useful for modulating an immune response in a subject having an immune-related disorder. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating an immune response in a subject having an immune-related disorder, e.g. arthritis by administering an antigen-specific epitope a cytokine or an agent that effects cytokine activity or expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; dermatological; antipsoriatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. coli DnaJpl antigen-specific epitope peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-2003
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11-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 9; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albani S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to a novel method for modulating an immune response subject having an immune-related disorder. The method comprises: (a)
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2001US-0339284P.
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Pred. No.
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Sequence 15

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RESULT 8
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                                                                                                                                                               contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MHC) ligand (Ia); (c) method for in vitro diagnosis of diseases associated with the presence (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunembalator, endocrine, antiallexpic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g., immune disorders, e.g.,
                                                                  immune deficiency, autoimmune states, hypersensitivity, allergy, graft rejection, infection, hormonal disorders and central nervous system diseases), also, where (I) is a MHC ligand (Ia), in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections; or (ii) of cancers. A particular application is in antimelanoma vaccines. (I) are also useful for in vitro diagnosis of diseases.
                       associated with interactions between MHC and (I), e.g. immunodeficiency virus infection. AAM98898 to AAM99592 which can be used in pharmaceutical compounds from the
                                                                                                                                                                                                                                                                                                                                                                                                                                    Stabilized pharmaceutical glutamine, useful e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glutamic acid; glutamine; vaccine; major histocompatibility comp
immunomodulator; antiallergic; endocrine; neuroprotectant; viruc
bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
pharmaceutical; immune disorder; immune deficiency; autoimmune;
hypersensitivity; allergy; graft rejection; infection; hormonal
central nervous system disease; cancer; melanoma; anti-melanoma
                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-611470/70
                                                                                                                                                                                                                                                                                                                                                         The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klinguer-Hamour C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200170772-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine related MHC ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FABR ) FABRE MEDICAMENT SA PIERRE
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                                                                                                                                                                                                                                                                                                                                                                                                                        strong
                                                                                                                                                                                                                                                                                                                                                                                    9; Page 107; 149pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                    invention describes a pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-FR000872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                containing N-terminal glutamic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-melanoma vaccines, is an addition salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide SEQ ID NO:447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beck A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                  compound (I)
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                                                      agnosis of diseases melanoma and human
                                       represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virucidal;
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                                                                                                                                                       graft
                                                                                                                                                                                                                                                   (c) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC
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Sequence 16 AA,

Query Match Best Local

Similarity

100

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Score Pred.

81; No.

DB 5; 1.1e-07;

Length

Sequence

16

AA,

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This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immunomodulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The creducing/inhibiting) an immune response in a subject having an immunogenic peptide is useful for modulating (i.e. augmenting/inducing or reducing/inhibiting) an immune response in a subject having an immune response in a subject having an inflammatory bowel disease or cancer. The immunogenic peptide of the creducing inflammatory bowel disease or cancer. The immunogenic peptide of the creducing horse, is also useful for modulating immunoeffector cell responsiveness in a subject. The immunogenic peptide is particularly cuseful for treating the above-mentioned diseases in mammals, e.g. cat, code, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal tolerisation, an experimental code immunisation. The present sequence represents an E. coli DNAJ immunogenic peptide of the invention
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans, e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory
                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 55; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martini A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2000; 2000US-0245181P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; arthritis; articular juvenile idiopathic arthritis; infectious disease; inflammatory bowel disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.Coli DNAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-489999/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
Sytostatic; antiinflammatory; antibacterial; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                  disease or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARTINI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tolerisation; DNA vaccination; anergy induction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albani s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 immunogenic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Pred. No. 1.1e-07;
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RESULT 10
RABSULT 10
ABRESTS 126
ID ABRESTS 126
AC 
RESULT 11
AAU02075
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                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for modulating an immune response in a subject having an immune-related disorder. The method comprises: (a) administering an antigen-specific epitope, where administration provides epitope-specific T cell immune modulation; and (b) administration provides cytokine, an agent that effects cytokine activity or expression, or an anticytokine therapy. The method of the invention has antiarthritic, antidiabetic, neuroprotective, anti-inflammatory, cytostatic, antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-ulcer, antianaemic, cardiant, respiratory general, antiallergic, dermatological, and antipsoriatic activity. The method is useful for modulating an immune response in a subject having an immune-related disorder. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating an immune response in a subject having an immune-related disorder, e.g. arthritis by administering an antigen-specific epitope and a cytokine or an agent that effects cytokine activity or expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarthritic; antidiabetic; neuroprotective; anti-inflammatory; cytostatic; antithyroid; anti-asthmatic; immunosuppressive; antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-430097/40.
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11-DEC-2001; 2001US-0339284P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiallergic; dermatological; antipsoriatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. coli dnaJ61 antigen-specific epitope peptide
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                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S, Martins A;
                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                        QKRAAYDQYGHAAFE 15
                                                                                                                                                                                                                                                                                                                                                                       16 AA;
                                                                                                                             QKRAAYDQYGHAAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 9; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                            Score 81; DB 6;
Pred. No. 1.1e-07;
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                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                         Length 16;
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Best Local S
                                                                                                                                                               The sequence represents shHSP/RA containing immunogenic epitope clusters (IEC) from Mycobacterium tuberculosis heat shock protein 65. Escherichia coli DNA J and human heat shock protein 60. The synthetic human target autoantigen genes of the invention comprise sequences coding for at least 2 IECs of autoantigen(s) related to a specific autoimmune disease. The synthetic human target autoantigen genes are useful for treating autoimmune diseases such as multiple sclerosis, insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis, uveitis, autoimmune hepatitis, thyroiditis, insulitis, orchitis, idiopathic thrombocytopenic purpura, and inflammatory diseases (Crohn's disease, ulcerative colitis). The synthetic human target autoantigen genes are also useful for diagnosis and/or monitoring the progression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shGLP/RA; immunogenic epitope cluster; IEC; synthetic human 60kDa heat shock protein; HSP60; HSP65; EcoDNAJ; autoantigen; autoimmune disease; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; uveitis; autoimmune hepatitis; thyroiditis; insulitis; orchitis; idiopathic thrombocytopenic purpura; inflammatory disease; Crohn's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic autoantigen shHSP/RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis heat shock protein 65; Escherichia coli DNA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU02075 standard; protein; 118
                                                                                                                       Sequence 118
                                                                                                                                                       autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases such as multiple sclerosis, insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and u
                                                                                                                                                                                                                                                                                                                                                                                                                               Novel synthetic human target autoantigen gene useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ben-Nun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                                                                                                                                                                                                                       Claim 176;
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   99
                               μ.
                                                                            Similarity
QKRAAYDQYGHAAFE
                            OKRAAYDOYGHAAFE
                                                                                                                                                                                                                                                                                                                                                                      Fig 53; 182pp; English.
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                                                              Conservative
                                                                                                                         A,
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                                                           100.0%; Score 81; DB 4; 100.0%; Pred. No. 9.4e-07; tive 0; Mismatches 0;
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                                                                 Indels
                                                                                               118;
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                                                               Gaps
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RESULT 13
AAB74197
ID AAB7
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AC AAB
AC AAB
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AC AAB
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AAB11396
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                            naturally occurring eukaryotic polypeptide containing two or more cysteine units bound via a disulfide bridge which comprises cultivation of prokaryotic cells in the presence of arginine or an amide compound. The method is useful for the preparation of eukaryotic proteins e.g. proteases, interferons, protein hormones, antibodies or antibody
              Unidentified
                                     Molecular chaperone;
                                                               OmpA-J domain
                                                                                          29-MAY-2001
                                                                                                                                            AAB74197 standard;
                                                                                                                                                                                                                                                                                                               Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                               stimulating hormone). It is especially useful for preparing proteins with more than five disulfide bridges, e.g. recombinant plasmingen activator (rPA). The technique is simple and does not require in vitro aftertreatment, such as the removal of inclusion bodies, reduction or
                                                                                                                                                                                                                                                                                                                                                                                         proteases, interferons, protein hormones, antibodies or antibody fragments (e.g. a single chain FV fragment that binds to thyroid stimulating hormone). It is especially useful for preparing prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preparation of water-soluble eukaryotic bridges e.g. rPA, comprises cultivation presence of arginine or amide compound.
                                                                                                                                                                                                                                                                                                                                          naturization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 17; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1048732-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotic protein; protease; interferon; antibody; hormone;
disulfide bridge.
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                                                                                                                                                                                                                                                                         Local Similarity
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DB; AAC66072.
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                                                                                                                                                                                                                                QKRAAYDQYGHAAFE
                                                                                                                                                                                                                                                           Conservative
                                                                                       (first entry)
                                                            fusion protein
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                                                                                                                                           protein; 131 AA
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                                                                                                                                                                                                                                                                      100.0%;
                                    OmpA signal sequence; J domain; DnaJ
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                                                                                                                                                                                                                                                                         Score 81; I
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                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preparation of a water-soluble,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides with disulfide of prokaryotic cells in the
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Matches
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WPI; 2001-204356/21.
N-PSDB; AAF61191.
                                                                                                                                                            Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disulfide eukaryotic protein containing two or more cysteines linked by disulfide bridges. The method comprises co-expression and secretion into the periplasm of a molecular chaperone via an expression vector coding for the chaperone. The expression vector also encodes a signal sequence. The method is useful for producing a naturally folded eukaryotic protein such as an antibody, antibody fragment, interferon, protein hormone or a protease containing two or several cysteines linked by disulfide bridges The present sequence is a fusion protein composed of the OmpA signal sequence and the Johann of DnaJ. This sequence was used in the method
                                                           29-JUL-1999;
                                  (HOFF ) HOFFMANN LA
                                                                                  29-JUL-1999;
                                                                                                            21-FEB-2001.
                                                                                                                                    EP1077263-A1
                                                                                                                                                                                             Chaperone protein; periplasm; antibody production; interferon production; protease production.
                                                                                                                                                                                                                                    Expression
                                                                                                                                                                                                                                                            18-MAY-2001
                                                                                                                                                                                                                                                                                     AAB70767;
                                                                                                                                                                                                                                                                                                          AAB70767 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 14; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing naturally folded eukaryotic proteins e.g. antibodies, interferon, hormones or proteases that contain two or several c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-246712/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interferon, hormones or proteases that contain the contain of a molecular linked by disulfide bridges comprises co-expression of a molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ambrosius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to a method for production of a naturally
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                                                                                                                                                                                                                                                                                                                                                                                                                         L Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention
                                                                                                                                                                                                                                                                                                                                                                         QKRAAYDQYGHAAFE
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                                                           99EP-00114811.
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                                                                                                                                                                                                                                  pUBS520-pIN-J-domain protein.
                                    ROCHE
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No.
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RESULT 15
AAY7201.8
ID AAY72
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XX AAY72
XX Secre
KW Fusio
KW Heat
CX Esche
XX Eplo5
XX Eplo5
XX Eplo7
PA (HOFF
XX Ambrc
XX Ambrc
XX PI
PA N-PSI
XX WPI
PT Produ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel method for preparing a naturally folded eukaryotic polypeptide (I) that contains two or more disulfide-bridged Cys residues by culturing prokaryotic cells that contain an expression vector for (I) including a prokaryotic signal sequence at its N-terminus and a nucleic acid (II) that secretes a chaperone protein (III) into the periplasm. (I) is secreted into the periplasm or medium; the signal peptide is then cleaved and (I) isolated from the periplasm or medium. The method is used for production of antibody, interferon, protein hormone or protease. Expression of (III) increases the yield of (I). The method is simple and eliminates time-consuming in vitro processing operations such as dissolution of inclusion bodies, reduction and refolding. (III) protects (I) against agglomeration and promotes their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation of naturally folded eukaryotic proteins, e.g. antibodies, is simultaneous expression of a chaperone protein, allows simple recovery from periplasm or medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein; chaperone; interferon; protease; hormone; fusion protein; naturally folded protein; lac-Ipp promoter; DnaJ; heat shock protein; HSP; outer membrane protein A; OmpA; J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               refolding. (III) proceed natural conformation
                                                                                                                                                  Producing water-soluble, naturally folded, and secreted eukaryotic polypeptide, involves culturing prokaryotic cells containing an expression vector encoding the polypeptide in the presence of arginine or a specific compound.
                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. coli OmpA-J domain fusion protein encoded by pUBS520-pIN-J-domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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The patent discloses a method for the production of a water-soluble, naturally folded and secreted eukaryotic proteins in prokaryotic cells. The method involves culturing the prokaryotic cells, containing an

Example 3; Page 17; 35pp; English.

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cc expression vector encoding the desired protein and the prokaryotic signal cc sequence, in the presence of an additive, e.g., L-arginine. The signal cc sequence mediates the secretion of the desired protein into the periplasm, where folding of the protein takes place. The prokaryotic cell cc also contains an expression vector encoding a molecular chaperone, e.g., c DnaJ and heat shock protein 25 (HSP25). The simultaneous co-overexpression and co-secretion of molecular chaperones in the periplasm in crecombinantly produces a high yield of eukaryotic secreted proteins in c prokaryotes. The method is useful for producing eukaryotic proteins such case an antibody, antibody fragment, interferon, protein hormone or a protease. The present sequence is an Escherichia coli outer membrane cc protein A (OmpA) signal sequence-J domain fusion protein encoded by corotein A (OmpA) signal sequence-J domain fusion protein encoded by the lac-Ipp promoter and the Ipp terminator. The periplasmic co-secretion coli of the DnaJ, facilitates the colling of the desired scores.
Sequence 131 AA;
                                                        folding of the desired secreted protein
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84 OKRAAYDOYGHAAFE 98

OKRAAYDOYGHAAFE 15 Conservative

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Matches Query Match Best Local

15;

Similarity

100.0%; Score 81; DB 4; 100.0%; Pred. No. 1.1e-06;

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Length 131; Indels

Search completed: August 17, 2004, Job time : 53 secs 22:23:11

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Title:
Perfect score:
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                                Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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POSSIBLE FUNCTION. POSSIBLE FUNCTION. MEDLINE=91187894; PubMed=1826368; Liberek K., Marszalek J., Ang D., Georgopoulos C., Zylicz M.; Liberek K., Marszalek J., and GrpE heat shock proteins jointly stimulate "Escherichia coli Dnad and GrpE heat shock proteins jointly stimulate ATPase activity of DnaK."; Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991). [6]	SEQUENCE FROM N.A. STRAIN-K12 / MG1655; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=K12; STRAIN=92334977; PubMed=1630901; YURA T., MORI H., Nagai H., Nagata T., Ishihama A., Fujita N., YURA T., Mizobuchi K., Nakata A.; 'Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region."; Nucleic Acids Res. 20:3305-3308(1992).	MEDLINE 8611189; PhiMed=3003084; Ohki M., Tamura F., Nishimura S., Uchida H.; Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the gene product."; J. Biol. Chem. 261:1778-1781(1986). [2] SEQUENCE FROM N.A. STRAIN=K12; MEDLINE=86111850; PubMed=3003085; Bardwell J.C.A., Tilly K., Craig E., King J., Zylicz M., Georgopoulos C.; "The nucleotide sequence of the Escherichia coli K12 dnaJ+ gene. A gene that encodes a heat shock protein."; J. Biol. Chem. 261:1782-1785(1986).	IT 1 PROCLI NAJ ECOLI STANDARD; PRT; 3 P08622; 01-AUG-1988 (Rel. 08, Created) 15-DEC-1998 (Rel. 37, Last sequence up 28-FEB-2003 (Rel. 41, Last annotation Chaperone protein dnaJ (Heat shock pro DNAJ OR GROP OR B0015. Escherichia coli. Bacteria; Proteobacteria; Gammaproteob Enterobacteriaceae; Escherichia. NCBI TaxID=562; ECUTENCE FORK N. 1000

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InterPro; IPR001623; D
InterPro; IPR008971; H
InterPro; IPR003095; H
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MEDILINE-20351465; PubMed=10891270;

Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;

"Solution structure of the cysteine-rich domain of the Escherichia coli chaperone protein DnaJ.";

J. Mol. Biol. 300:805-818(2000).

-!- FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN COMPLEX AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY WITH GRPE, THE ATPASE ACTIVITY OF DNAK.
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MEDLINE=96291434; PubMed=8764403;

Pellechia M., Szyperski T., Wall D., Ge
"NMR structure of the J-domain and the
"Scherichia coli DnaJ chaperone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PDB; 18Q0; 15-JUN-99.
PDB; 118Q2, 15-JUN-99.
PDB; 1EXK; 26-JUL-00.
ECO2DBASE; H036.5; 6TH EDITION
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Pfam; PF00684; DnaJ CXXXGXG;
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
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PROSITE; PS00637; DNAJ_CXXCXGXG;
Chaperone; DNA replication; Heat
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P48206;
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                    STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur
Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducreyi.";
Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases
                                                                                                                                                                                                                                                                                                                Pasteurellaceae; Haemophilus
NCBI_TaxID=730;
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                                                                                                                                               SEQUENCE FROM N.A.
  FUNCTION: Acts as a co-chaperone.
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RESULT 3
DNAJ SALTY
ID DNAJ S
AC Q60004
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DT 15-DEC
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DE Chaper
GN DNAJ G
OS Salmon
OC Bacter
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Matches 15
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01-NOV-1997
15-DEC-1998
10-OCT-2003
                                                                                                Salmonella typhimurium, Salmonella typhi.
                                                                                                                                        Chaperone protein dnaJ.
DNAJ OR STM0013 OR STY0013
    SEQUENCE
                                  NCBI_TaxID=602,
                                                              Enterobacteriaceae;
                                                                                 Bacteria; Proteobacteria;
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PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
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Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGXG;
PFINTS; PR00625; DNAJPROTEIN.
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InterPro; IPR001623; DnaJ N.
InterPro; IPR003095; Hsp_DnaJ.
Pfam; PF00226; DnaJ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chaperone;
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COFACTOR: Binds 2 zinc ions per monomer (By simila
SUBCELLULAR IOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the dnaU family.
SIMILARITY: Contains 1 J domain.
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CXXCXGXG MOTIF.

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Pfam;
Pfam;

Pfam;

PF00226;

DnaJ;

Hsp_DnaJ

DnaJ_C; 1.
DnaJ_CXXCXGXG;

InterPro; IPR002939; InterPro; IPR001305; InterPro; IPR001623; InterPro; IPR008971; EnterPro; IPR003095; EnterPro;

DnaJ_C.
DnaJ_CX
DnaJ_N.
HSP40_D

CXXCXGXG. N. DnaJ_pep StyGene; SG10620; dnaJ

HSSP;

P08622; 1EXK

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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.", Nature 413:848-852(2001).
                                            EMBL;
                                                                                                                                                                                                the
                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Meng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Spieth J., Courtuey L., Porwollik S., Ali J., Dante l Leonard S., Nguyen C., Scott K., Holmes A Ryan E., Sun H., Florea L., Miller W., Stwaterston R., Wilson R.K.;
                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                 entities requires a license agreement
                                                                                                                                                     modified
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                                                                                                                                                                                                                      between
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Stephen R.J., Hinton J.
Submitted (JUN-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.typhimurium; STRAIN=LT2
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 185:2330-2337(2003).
- FUNCTION: INTERACTS WITH DNAK, TO DISASSEMB AT THE PHAGE LAMBDA CRIGIN OF REPLICATION.
WITH GRPE, THE ATPASE ACTIVITY OF DNAK.
                                                                                                                                                                                                                                                                          PROTEIN (BY SIMILARITY).
SIMILARITY: Belongs to the dnaJ f.
SIMILARITY: Contains 1 J domain.
SIMILARITY: Contains 1 CR domain.
                                                                                                                                                                                           ween the Swiss Institute of Bioinfo
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By simil INDUCTION: BY HEAT SHOCK UNDER THE CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: Binds 2 zinc ions per monomer
                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is producen the Swiss_Institute_of Bioinformatics
U58360; AAB02911.1; --
AE008693; AAL18977.1;
AL627265; CAD01166.1;
AE016834; AA067747.1;
                                                                                                                                                   non-profit institu
and this statement
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                                                                                                                                                                                                                                                                                                                         family.
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Mulvaney E.
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PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
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Pasteurellaceae; Haemophi
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=727;
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                                                                                                                       TUNCTION: Acts as a co-chaperone. Stimulates, jointly with ATPase activity of dnak (By similarity). COFACTOR: Binds 2 zinc ions per monomer (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the dnad family.

SIMILARITY: Contains 1 domain.

SIMILARITY: Contains 1 CR domain.
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MEDLINE-98182595; PubMed=9522128;
Yoshida A., Nakano Y., Yamashita Y., Yu H., Ohishi M., Koga T.;
"Isolation and characterization of the dnakJ operon from
Actinobacillus actinomycetemcomitans.";
DNA Seq. 8:93-98(1997).
-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with the ATPase activity of dnak (By similarity).
-!- COFACTON: Binds 2 zinc ions per monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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034242; Q9KTP5;
15-JUL-1998 (Rel. :
16-OCT-2001 (Rel. :
16-OCT-2001 (Rel. :
SEQUENCE FROM N.A.

STRAIN-E1 Tor N16961 / Serotype 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
                                                                                       Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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                                                                                                                        Chaperone protein DNAJ OR VC0856.
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                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002939; Dnau_C.
InterPro; IPR001305; Dnau_CXC
InterPro; IPR001623; Dnau_N.
InterPro; IPR008971; HSP40_Dnau
InterPro; IPR003095; Hsp_Dnau.
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SIMILARITY: Contains 1 J domain.
SIMILARITY: Contains 1 CR domain.
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                                                                                                                                                                                                                                                                                                     Similarity
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PS50076; DNAJ_2; 1.
PS00637; DNAJ_CXXCXGXG;
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J_CXXCXGXG.
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CCPD286756FF44E1 CRC6-
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                                                                                                                                              update)
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McDonald L., Ut
Salzberg S.L.,
Fraser C.M.;
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STRAIN-Classical 569B / ATCC 25870
MEDLINE-99150229; PubMed=10024539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Vibrio cholerae."
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FUNCTION: Acts as a co-chaperone. Stimulates, jointly we the ATPase activity of dnak (By similarity).

COFACTOR: Binds 2 zinc ions per monomer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: Belongs to the dnad family.

SIMILARITY: Contains 1 J domain.

SIMILARITY: Contains 1 CR domain.
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L., Utterback T., Fleischmann R.
S.L., Smith H.O., Colwell R.R.,
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anos J.J.,
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entities requires a license agreement (S or send an email to license@isb-sib.ch). European Bioinformatics Institute. SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL non-profit institutions as long and this statement is not removed. noved. Usage by and for commercial
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Pfam; PF06884; DnaJ C; CXCCXGXG;
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
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PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
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InterPro; IPR001305; Dnad_CXXCXGXG.
InterPro; IPR001623; Dnad_N.
InterPro; IPR008971; HSP40 Dnad_per
InterPro; IPR003095; Hsp_Dnad_
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EMBL; Y14237; CAA74628.1; -
PIR; D82270; D82270.
HSSP; P08622; 1BQZ.
TIGR; VC0856; -
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-:- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPses activity of dnak (By similarity).

-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the dnaJ family.

-!- SIMILARITY: Contains 1 J domain.
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Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGXG; 1.
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PROSITE; PS00636; DNAJ-
PROSITE; PS50076; DNAJ-
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                            SMART;
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InterPro; IPR008971; HSP40 Dna
InterPro; IPR003095; Hsp_DnaJ.
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"Cloning and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrionaceae; Vibrio.
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SM00271; DnaJ; 1.
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Pred. No. 2.5e-06;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Best Local S
Matches 14
PROSITE; PS00636; DNAJ_1; 1.

PROSITE; PS00637; DNAJ_2; 1.

PS00637; DNAJ_2; 1.

PS00637; DNAJ_2; 1.

PS00637; DNAJ_2; 1.

J-DOMAD_2; 1.

J-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001305; DnaJ_CXXCXGXG.
InterPro; IPR001623, DnaJ_N.
InterPro; IPR008971; HSP40 DnaJ_pep.
InterPro; IPR003095; Hsp_DnaJ.
Pfam; PP00226; DnaJ; 1.
Pfam; PF000226; DnaJ; 2XXCXGXG; 1.
Pfam; PF000684; DnaJ_CXXCXGXG; 1.
PR.NYTS; PR006525; DNAJ_PXOTEIN.
SNART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpkins S.A., Johnston A.W.B., James R.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with ATPase activity of dnaK (By similarity).
-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the dnaJ family.
-!- SIMILARITY: Contains 1 J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence
16-OCT-2001 (Rel. 40, Last annotat:
Chaperone protein dnaJ (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium leguminosarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y14649; CAA74983.1; -. HSSP; P08622; 1BQZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=8401:PRL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria;
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41619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Latement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.3%;
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Pred. No. 2.6e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  (CXG; 1.
Heat shock; Repeat; Zinc; Metal-binding
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ZINC 1 (BY SIMILARITY).
; ABA1B52321D15F58 CRC64;
                                                                                                                                                                                                                                                           CXXCXGXG
                                                                                                                                                                                                                                                                                     CXXCXGXG
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                                                                                                                                                                                                                                                                                                                                                     J-DOMAIN.
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EXG MO
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. 2.6e-06; ...
0; Indels
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Best Local S
Matches 14
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Best Local S
Matches 14
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01-AUG-1992 (Rel. 2
16-OCT-2001 (Rel. 4
Nolc protein.
                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P26508;
01-AUG-1992
                                                                                                                        Chaperone;
                                                                                                                               PROSITE; PS00636; DNAJ 1; 1. PROSITE; PS50076; DNAJ 2; 1.
                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium fredii (Sinorhizobium fredii).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
NON_TER
                                                                                                                                                                        Pfam; PF00226; DnaJ; Pfam; PF01556; DnaJ
                                                                                                                                                                                         InterPro; IPR002939; DnaJ C.
InterPro; IPR001623; DnaJ N.
InterPro; IPR008971; HSP40 D
InterPro; IPR003095; Hsp_Dna
                                                                                                                                                                                                                                                                                                    modified and this statement
                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                "noll, a Rhizobium fredii gene involved in cultivar-specific nodulation of soybean, shares homology with a heat-shock gen Mol. Microbiol. 5:737-745(1991).
-!- SIMILARITY: Contains 1 J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHIFR
                                                                                                                                                       PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                        HSSP; P08622; 1BQZ.
                                                                                                                                                                                                                                                 PIR; S15295; S15295.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91260457; PubMed=1646377;
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=USDA 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           Krishnan H.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHIFR
 60
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                                        . Similarity
14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                an H.B., Pueppke S.G.;
a Rhizobium fredii gene
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QKRAAYDRYGHAAFE
                 QKRAAYDQYGHAAFE 15
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                                                                                                            S500,0,; Nodulation.
                                                                               392 AA;
                                       Conservative
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23,
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234
                                                95.1%;
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93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
74
                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                      DnaJ pep.
                                      Score 77; DB Pred. No. 3.9e 1; Mismatches
                                      ۲.
                                                                                                 J-DOMAIN.
GLY-RICH.
                                                                                                                                                                                                                                                                                                    is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77;
Pred. No.
                                                                                          ARG-RICH
                                                                              B60F6DB27980F324 CRC64;
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ДВ)
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                                                          DB 1;
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SIMILARITY)
                                                .9e-06;
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                                                         Length 392;
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RESULT 10
   Best Local
Matches
                         Query Match
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
28-FEB-2003 (Rel. 4
                                                                       METAL
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                                                                                                                                               REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                                                                                    SMART; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS00637; DNAJ CXXCXGXG;
                                                                                                                                                                                                                                                                                 PRINTS; PROUBZ, ....; SMART; SM00271; DnaJ; SMART; DNA;
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                  SEQUENCE
                                                                                                                                                                                                                                 Complete
                                                                                                                                                                                                                                                                                                               Piam; PF01556; DnaJ_C; 1.
Piam; PF00684; DnaJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00226; DnaJ;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE006111;
HSSP; P08622; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with g the ATPase activity of dnaK (By similarity).
-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
-!- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the dnaJ family.
-!- SIMILARITY: Contains 1 J domain.
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STRAIN=Pm70;
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                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001623; DnaJ N. InterPro; IPR008971; HSP40 I
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002939;
InterPro; IPR001305;
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Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNAJ OR PM0740
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               Similarity
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                                                                                                                                                                                                                                proteome
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                                                                                                                                                                                                                                           DNA replication;
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   Conservative
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DnaJ_CXXCXGXG.
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Last annotation update)
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                                                      GLY-RICH
CXXCXGXG MOTIF.
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
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             Score 75; I
Pred. No. 8.
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  Mismatches
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                      Length 372;
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032465;
30-MAY-2000
16-OCT-2001
28-FEB-2003
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MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 407:81-86(2000).

-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly withe ATPase activity of dnak (By similarity).
-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
-!- SUBUBLICHAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELUTLAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCILITARITY: Belongs to the dnaJ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato S., Ishikawa H.; "Structure and expression of the dnaKJ operon of Buchnera, intracellular symbiotic bacteria of aphid.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gar
Enterobacteriaceae; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
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                             DOMAIN
DOMAIN
                                                                                                                                                            Pfam; PF00226; DnaJ; 1.
Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGXG; 1.
                                                                                                                                                                                                  InterPro; IPR002939; DnaJ_C.
InterPro; IPR001105; DnaJ_CXCXGXG.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR008971; HSP40_DnaJ_pep.
InterPro; IPR003095; Hsp_DnaJ.
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                                                                                                   PROSITE; PS00636; DNAJ_PROSITE; PS50076; DNAJ_
                                                          Complete
                                                                                                                                PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                HSSP;
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             REPEAT
                                                                                        PROSITE; PS00637;
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P08622; 1BQZ.
                                                          proteome
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(Rel. 40, Last sequence up
(Rel. 41, Last annotation
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162
                                                                        replication;
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                                                                                                ; DNAJ_1; 1.
DNAJ_2; 1.
                                                                                        DNAJ CXXCXGXG;
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152
169
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                                                                        Heat shock;
J-DOMAIN.
GLY-RICH.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
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                                                                        Repeat;
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                                                                        Zinc; Metal-binding;
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RESULT 12
DNAJ_BUCAP
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MEDLINE=22084549; bubMed=12089438;

MEDLINE=22084549; bubMed=12089438;

A Tamas I, Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,

A Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;

"50 million years of genomic stasis in endosymbiotic bacteria.";

"50 million years of genomic stasis in endosymbiotic bacteria.";

"50 million years of genomic stasis in endosymbiotic bacteria.";

"50 million years of genomic stasis in endosymbiotic bacteria.";

"50 million years of genomic stasis in endosymbiotic bacteria.";

"61 public years of genomic stasis in endosymbiotic bacteria.";

"62 ci- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

the ATPasse activity of dnak (By similarity).

"62 ci- SUBUNIT: Homodimer (By similarity).

"63 public years of genomic stasis (By similarity).

"64 public years of genomic stasis (By similarity).

"65 public years of genomic stasis (By similarity).

"67 public years of genomic stasis (By similarity).

"68 public years of genomic stasis (By similarity).

"69 public years of genomic stasis (By similarity).

"60 public years of genomic stasis (By similarity).

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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                        Pfam; PF00226; DnaJ; 1.
Pfam; PF00556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXXG; 1.
                                                                                                                                                   InterPro; IPR002939; Dnad_C.
InterPro; IPR001305; Dnad_CXXCXGXG.
InterPro; IPR001623; Dnad_N.
InterPro; IPR008971; HSP40_Dnad_per
InterPro; IPR003095; HSp_Dnad_.
Dfac. DF00236: Dnad_1 1.
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28-FEB-2003
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PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
                                                                                                                                                                                                                                                                        EMBL; AE014090; AAM67713.1; ~.
                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
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86.7%;
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CXXCXGXG MOTIF.

ZINC 1 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

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Pred. No. 8.5e-06;
2; Mismatches 0
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RX MEDLINE=2022256; PubMed=10761919;
RA A Riee S.R., Morelli G., Basham D., Bentley S.D., Churche A Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., I A Jagels K., Leather S., Moule S., Mungall K., Quail M.A., A Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., A Whitehead S., Spratt B.G., Barrell B.G.;
T "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
Nature Annaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 13
                          Science
                                                     Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelsc Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Oclark Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., "Complete genome sequence of Neisseria meningitidis serogroup E.""
                                                 "Complete MC58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAJ NEIMA
P57107;
16-OCT-2001
                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-MC58 / Serogroup B;
MEDLINE-20175755; PubMed-10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                 Chaperone protein dnaJ.
DNAJ OR NMA0209 OR NMB0059.
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SEQUENCE
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Neisseria meningitidis (serogroup
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=65699,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00637;
FUNCTION: Acts as a co-chaperone. Stimulates, jointly with the APPase activity of dnaK (By similarity). COFACTOR: Binds 2 zinc ions per monomer (By similarity).
                                                                                                                                                                                                            404:502-506(2000).
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13; Conser
                                      287:1809-1815(2000).
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86.7%;
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CXXCXGXG MOTIF:
CXXCXGXG MOTIF:
CXXCXGXG MOTIF:
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
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ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
EB73F48DAF7A2D34 CRC64;
                                                                                                                                                                                                                                 serogroup A strain of Neisseria
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No.
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own D., Chillingworth T.,
eltwell T., Hamlin N., Holroyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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H., Clark E.
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Pfam; PF00556; DnaJ C; 1.
Pfam; PF00684; DnaJ C; 1.
Pfam; PF00684; DnaJ CXCXGXG; 1
PRINTS; PR00625; DNAJ PROTEIN.
SWART; SW00271; DnaJ; 1.
PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS00637; DNAJ 2; 1.
PROSITE; PS00637; DNAJ CXXCXGXG
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
REPEAT
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InterPro; IPR001305; DnaJ_C.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR003095; Hsp_DnaJ_pep
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EMBL;
PIR; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                             SEQUENCE
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Complete p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; NMB0059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELULIAR LOCATION: Cytoplasmic (By similarity)
SIMILARITY: Belongs to the dnau family.
SIMILARITY: Contains 1 J domain.
SIMILARITY: Contains 1 CR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; AL162752; CAB83522.1;
; AE002365; AAF40528.1;
D81242; D81242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
  61
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                                     1 OKRAAYDOYGHAAFE
                                                                               13;
                                                                                                  Similarity
  EKRAMYDQYGHAAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome.
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147
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167
                                                                               Conservative
                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNAJ_2; 1.
DNAJ_CXXCXGXG;
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117
154
171
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193
207
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164
167
186
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86.7%;
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                                                                         Score 73; DB 1;
Pred. No. 1.9e-05;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                   CXXCXGXG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shock; Repeat;
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(BY SIMILARITY).

(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                               Length 373;
                                                                                                                                                           CRC64;
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Q05980;
01-FEB-1994
01-FEB-1994
16-OCT-2001
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BRUOV
DNAJ_F
                   Brucella ovis.
Bacteria; Proteobacteria;
Brucellaceae; Brucella.
             NCBI_TaxID=236;
                                                  Chaperone
                                                                                      BRUOV
                                                994 (Rel.
994 (Rel.
)01 (Rel.
protein
                                                                                      STANDARD;
                                                        28, Creat
28, Last
40, Last
                                                  dnaJ
                                                                       Created)
                           Alphaproteobacteria; Rhizobiales;
                                                               sequence update)
                                                         annotation
                                                                                     375
                                                         update
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DNAJ AGRT5
ID DNAJ AGRT5
ID DNAJ AGRT5
AC P50018;
DT 01-OCT-1996
DT 28-FEB-2003
DT 28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DnaK functionally expressed in Escher:
J. Bacteriol. 174:8036-8042(1992).
-i- FUNCTION: Acts as a co-chaperone.
                                                                                                                                                                                                                  METAL
METAL
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SEQUENCE
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Pfam; PF01556; DnaJ C; 1.
Pfam; PF00684; DnaJ CXXCXGXG; 1.
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the ATPase activity of dnaK (By similarity).
-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sri Widada J.; "Cloning and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sri Widada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 25840 / 63/290T;

MEDLINE=93094135; PubMed=1459952;

Celler M.F.M., Teyssier J., Nicolas
                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
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METAL
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PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637, DNAJ_CXXCXGXG;
Chaperone; DNA replication; Heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002939; DnaJ C.
InterPro; IPR001305; DnaJ CX.
InterPro; IPR001623; DnaJ N.
InterPro; IPR008971; HSP40 D
                                                                                                                                                                                                                                                                                                                                                                                             Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; B47042; B47042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: By heat shock.
SIMILARITY: Belongs to the dnaJ family.
SIMILARITY: Contains 1 J domain.
SIMILARITY: Contains 1 CR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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                                                                                                                                                                                Similarity
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86.7%;
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 Last sequence update)
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                          Created)
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CXXCXGXG
ZINC 1 (B
ZINC 1 (B
ZINC 2 (B
ZINC 1 (E
ZINC 1 (E
                                                                                                                                                                             Score 73; DB 1;
Pred. No. 1.9e-05;
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CCXGXG MOTIF.
CCXGXG MOTIF.
CC 1 (BY SIMILARITY).
CC 1 (BY SIMILARITY).
CC 2 (BY SIMILARITY).
CC 2 (BY SIMILARITY).
CC 2 (BY SIMILARITY).
CC 2 (BY SIMILARITY).
CC 1 (BY SIMILARITY).
CC 1 (BY SIMILARITY).
CC 1 (BY SIMILARITY).
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                                                                                                                                                                   Gaps
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Pfam; PF00226; DnaJ; Pfam; PF01556; DnaJ (Pfam; PF00684; DnaJ

DNAJPROTEIN.

CXXCXGXG;

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InterPro; IPR002939; Dnad C.
InterPro; IPR001305; Dnad CXXCXGXG.
InterPro; IPR001623; Dnad N.
InterPro; IPR003095; Hsp_DnaJ.

PIR; AD2591; AD2591. PIR; D97373; D97373. PIR; I39586; I39586.

HSSP; P08622; 1BQZ.

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MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almedda N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Katyavin C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 177:5952-5958(1995).

-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with the ATPase activity of dnak (By similarity).
-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- INDUCTION: By heat shock.
-!- SIMILARITY: Belongs to the dnaJ family.
-!- SIMILARITY: Contains 1 J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizo
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobac
                                                                                                                                                                                                                               EMBL; AE008986; AAL41146.1; -. EMBL; AE007953; AAK85941.1; -. EMBL; X87113; CAA60593.1; -.
                                                                                                                                                                                                                                                                                                         entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collak between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The dnaKJ operon of Agrobacterium tumefaciens: transcriptional analysis and evidence for a new heat shock promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-66 FROM N.A. MEDLINE=96011387; PubMed=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21608550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=176299;
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DNAJ OR ATU0121 OR AGR_C_192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G., Ron E.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294:2317-2323 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7592349;
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DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00635; DNAJ 2; 1.

DR PROSITE; PS00637; DNAJ 2; 1.

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